

1 AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCTGTGCTGCTGACCTTACAAGATGCCA AGAGAAGATGCTCACTTCTATCTATGGTTAC CCCAAGAGGGGCACGGCCACTCTTACACC 119
 22 MetPro ArgGluAspAlaHisPheIleTyzGlyTyr ProLysLysGlyHisGlyHisSerTyzThr 22
 239 62 ACGGCTGAAGAGGCGCTGGGATCGGCATC CTGACAGTATCTCTGGAGTCTTACTGCTC ATCGCTGTGGTATTTGTAGAAGCAAAAT GGATACAGAGCCTTGTGATGGATATAAAGTCTT 239
 ThrAlaGluGluAlaAlaGluVilleglVilLeuThrValIleIleGluVilLeuLeuLeu IleGluCysValTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu 62
 359 102 CATGTTGGCACTCAATGTGCTTAAACAAGA AGATGCCCAACAAGAGGTTTGTATCATCGG GACAGCAAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCTCCCAATGCTCCACCT 359
 HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGlnGluGlyPheAspHisArg AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro 102
 479 118 GCTTATGAGAAACTCTCTGCAGACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG AGACACCTGAGACATGCTGAAATTAATTCT CTCACACTTTTGTCTTGAATTTAATACAGAC 479
 AlaTyzGluLysLeuSerAlaGluGlnSer ProProProTyzSerPro 118
 599 719 ATCTAATGTTCTCTTTGGATGGTGTAGG AAAATGCAAGCCATCTCTAATAATAAGTC AGTGTAAATTTTACTAGTCCGCTAGCA GTACTAATCAATGTGAGGAATGATGAGAAA 599
 TATTAATTTGGAAAACTCCATCAATAAAT GTTGCATGCATGATATCTGTGCCAGA GGTAAATGTTAGTAATTCATGGTGTATTT TCTGACAGACAGAAATCAAGTGGGTATCT 719
 959 1079 GGGGCCATCCATTTCTCTTTACTTGAAT TTGGCTAATAACAACTAGTCAAGTTTCG AACCTTGACCCACATGAACTGTACACAGAA TTGTCCAGTACTATGGAGTCTCACAAAG 959
 840 1199 GATACCTTTTACAGGTTAAGACAAGGTTG ACTGGCTATTATCTGATCAAGAACAATGT CAGCAATGCTCTTTGTGCTCTAAATTTCT ATTATACTACAAATAATATATTTGTAAGATC 1079
 960 1319 CTATAGCTCTTTTGTGAGATGGAGTTT CGCTTTTGTGCTCCAGCTGGAGTGCATG GGCATATGCTGCTTCTCCATGTTGGTCA TCCCAGGTTCAAGCAATTTCTCTGCCCTTAC 1199
 1080 1439 CTCTCTGAGTAGTGGGATTACAGCGTGC ATTACAGCGGTGAGCCACACGCTGGCT GGTATGATATCTTTAGGTAGACATATAAC GCAGTCTAAATTACATTTCACTTCAAGGCTC 1319
 1200 1559 AATGCTATTCTAATAATGACAGATTTT CTACTAAACCAGAAATTTGGTAGAGGATTT AAATAAGTAAAGCTACTATGTACTGCTTAAATG AGTGTCTGATGCTGTGTACTGCTTAAATG 1439
 1320 1559 TACCTATGGCAATTTAGCTCTCTTGGGTTG CCAAATCCCTCTCACAAAGATGTGCAGAG AAATCATAAAGCATCAGAGATTTCTGAATAA AAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIGURE 1

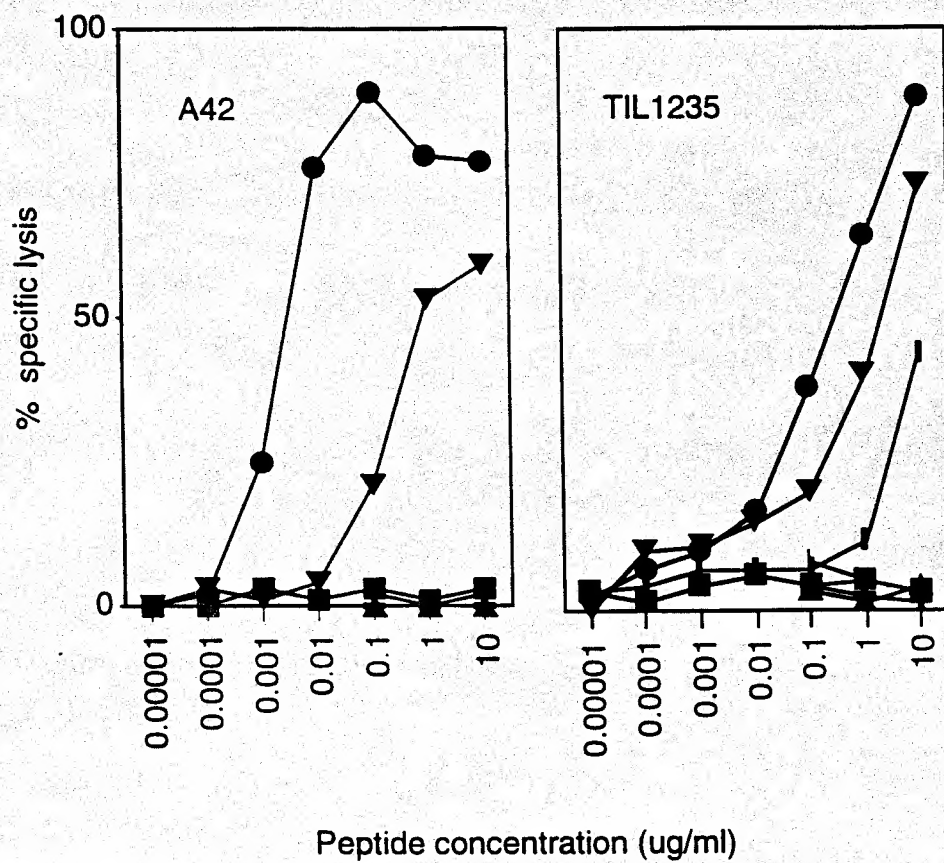


FIGURE 2

FIGURE 3A

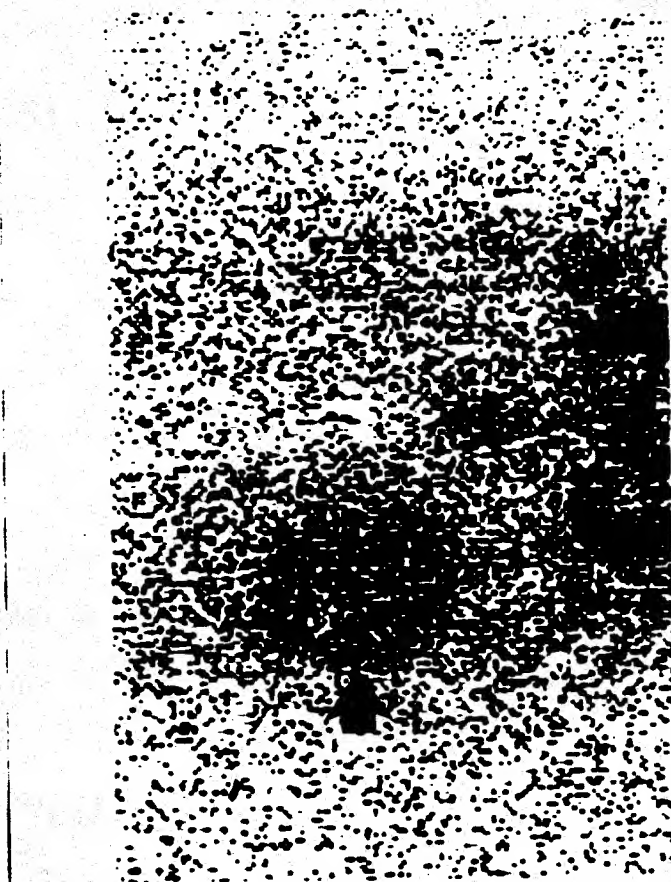
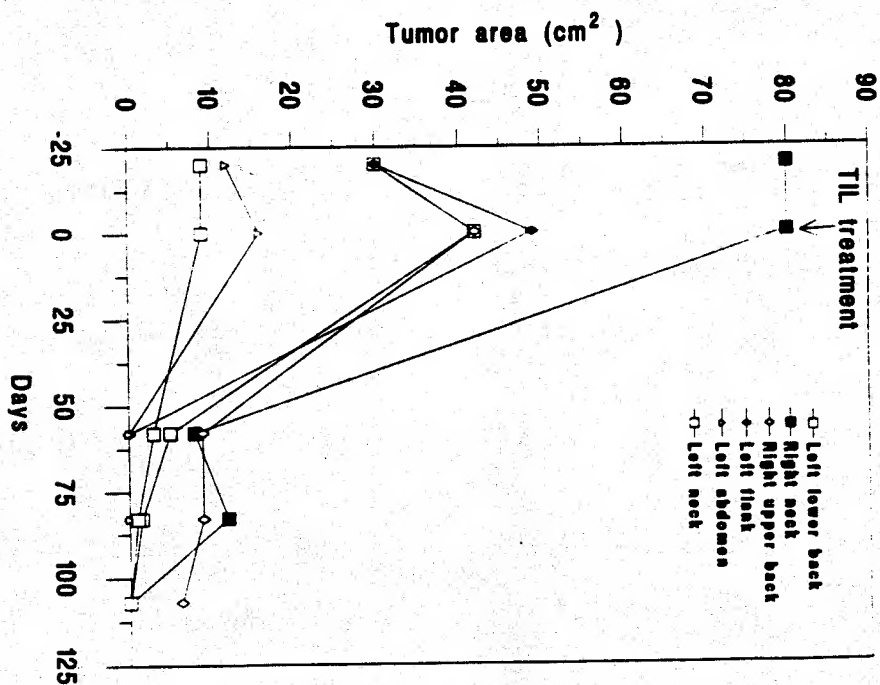


FIGURE 3B



GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
CCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGA CTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIGURE 4

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACCTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TCGGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIGURE 4 (continued)

FIGURE 5A

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1 MDLVLRCLL HLAIVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNROLYP
51 EWTEAQRDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKIWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251 LAEADLSYTW DFGDSSGTLI SRALVVTHY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVP GTT DHRPTAEAP NTTAGQVPTT EVVGTTPGA PTAEPSGTTS
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGS LGP LLDG TATLR LVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQPVLPSPAC
551 QLV LHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601 GILLVLMVV LASLIYRRRL MKQDFSVPL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

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FIGURE 5B

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Pme117 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----
gp100 M-----V-----Q-----L-----
cDNA25FL M-----F-----Q-----L-----
cDNA25TR Q-----L-----PPQWAAGLSTLI
1 162 236 274 588 649

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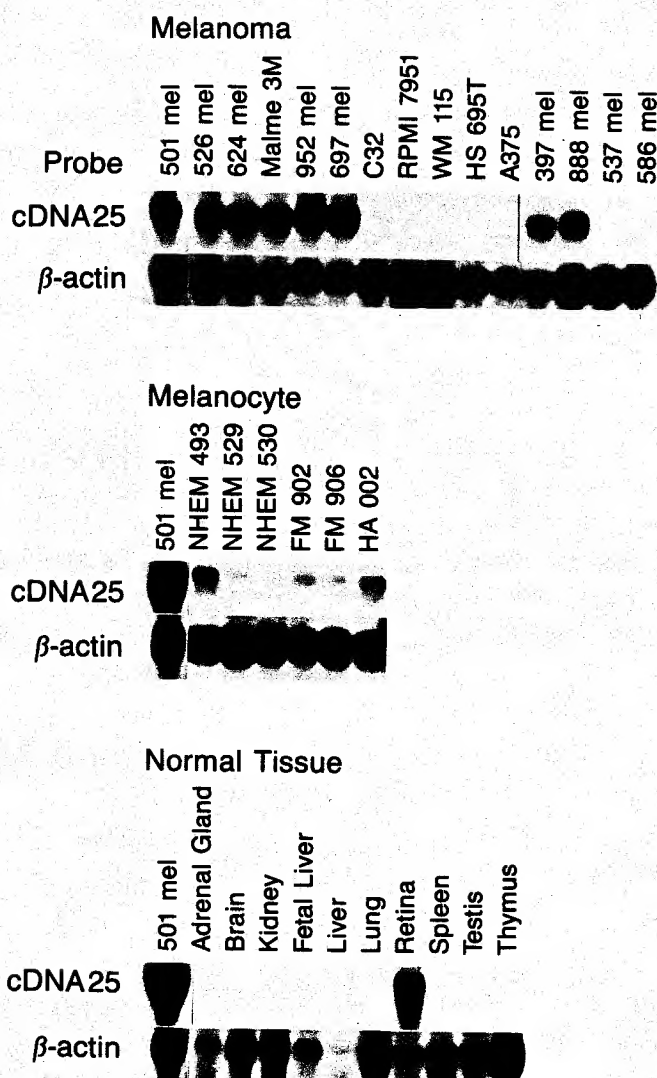


FIGURE 6